AUTHOR INDEX, VOLUME 54

Section	March	June	Sept.	Dec.
Acknowledgements	—	—	—	1685
The International Biometric Society	—	—	—	1689
Book Reviews	392	749	1197	1675
Corrections	399	—	1205	1684
Correspondence	389	788	1190	—

ASHBY, M. A. (see GILBERT, P. B.) 799

ANDERSON, A. B., and PRENTICE, R. L. On the accommodation of disease rate correlations in aggregate data studies o disease risk factors 1527

AZAÏS, J.-M., MONOD, H., and BAILEY, R. A. The influence of design on validity and efficiency of neighbour methods, 1374

BAILER, A. J. (see SEE, K.) 67

BAILEY, R. A. (see AZAÏS, J.-M.) 1374

BAKER, S. G. Evaluating the age to begin periodic breast cancer screening using data from a few regularly scheduled screenings 1569

BAKKE, Ø. (see ENGEN, S.) 840

BARNHART, H. X. and WILLIAMSON, J. M. Goodness-of-fit tests for GEE modeling with binary responses 720

BAUMGARTNER, W., WEIß, P., and SCHINDLER, H. A nonparametric test for the general two-sample problem 1129

BECKER, N. G. and HASOFER, A. M. Estimating the transmission rate for a highly infectious disease 730

BELISLE, P., JOSEPH, L., MacGIBBON, B., WOLFSON, D. B., and du BERGER, R. Chang-point analysis of neuron spike train data 113

BERGER, V. W., PERMUTT, T., and IVANOVA, A. Convex hull test for ordered categorical data 1541

BETENSKY, R. A. Construction of a continuous stopping boundary from an alpha spending function 1061

BETENSKY, R. A. Multiple imputation for early stopping of a complex clinical trial 229

BHANDARY, M. (see YOUNG, D. J.) 1363

BILLARD, L., DAYANANDA, P. W. A., and ELMES, S. Assessment of plant stress due to the presence of disease 877

BLAYLOCK, J. (see VARIYAM, J. N.) 1654

BLOCH, J. and CHAVANCE, M. A mixed model for repeated dilution assays 482

BOEHNKE, M. (see HAUSER, E. R.) 1238

BÖHNING, D., DIETZ, E., and SCHLATTMANN, P. Recent developments in computer-assisted analysis of mixtures 525

BORCHERS, D. L., BUCKLAND, S. T., GOEDHART, P. W., CLARKE, E. D., and HEDLEY, S. L. Horvitz–Thompson estimators for double-platform line transect surveys 1221

BORCHERS, D. L., ZUCCHINI, W., and FEWSTER, R. M. Mark–recapture models for line transect surveys 1207

BRACCI, P. M., BULL, S. B., and GRYNPAS, M. D. Analysis of compositional bone density data using log ratio transformations 337

BROOKMEYER, R. (see GRAY, S. M.) 976

BROSS, I. D. Correspondence 1190

BUCKLAND, S. T. (see BORCHERS, D. L.) 1221

BUIST, W. (see ENGEL, B.) 1155

BULL, S. B. (see BRACCI, P. M.) 337

BULLEN, L. (see PLEDGER, S.) 61

BURGE, H. (see HIGGINS, K. M.) 19

BUYSE, M. and MOLENBERGHS, G. Criteria for the validation of surrogate endpoints in randomized experiments 1014

CAIRNS, D. Correspondence 788

CANNON, R. M. Sampling to comply with a maximum pest limit 847

CARLIN, B. P., KADANE, J. B., and GEIFAND, A. E. Approaches for optimal sequential decision analysis in clinical trials 964

CARPENTER, D. O. (see DIRIENZO, A. G.) 493

CATCHPOLE, E. A., FREEMAN, S. N., MORGAN, B. J. T., and HARRIS, M. P. Integrated recovery/recapture data analysis 33

CAUSEUR, D. J. and DHORNE, T. J. Finite sample properties of a multivariate extension of double regression 1591

CHAO, E. C. Gibbs sampling for long-term survival data with competing risks 350

CHAPPELL, R. (see PAN, W.) 1053

CHAVANCE, M. A. (see BLOCH, J.) 482

CHEN, C.-L., POLLOCK, K. H., and HOENIG, J. M. Combining change-in-ratio, index-removal, and removal models for estimating population size 815

CHEN, M.-H., MANATUNGA, A. K., and WILLIAMS, C. J. Heritability estimates from human twin data by incorporating historical prior information 1348

CHEN, S. (see HUANG, X.) 1420

CHEN, S., COX, C., and CUI, L. A more flexible regression-to-the-mean model with possible stratification 939

CHEN, S. X. Measurement errors in line transect surveys 899

CHENG, S. C., FINE, J. P., and WEI, L. J. Prediction of cumulative incidence function under the proportional hazards model 219

CHEW, G. (see HIGGINS, K. M.) 19

CLARKE, E. D. (see BORCHERS, D. L.) 1221

COMMENGES, D. (see JOLY, P.) 185

COUTURIER, S. (see RIVEST, L.-P.) 865

COWLING, A. spatial methods for line transect surveys 828

COX, C. (see CHEN, S.) 939

COX, N. J. (see NICOLAE, D. L.) 1271
CRÉPEAU, H. (see RIVEST, L.-P.) 865
CROUCHLEY, R. and DASSIOS, A. Interpreting the beta geometric in comparative fecundability studies 161
CUI, L. (see CHEN, S.) 939
CULLIS, B., GOGEL, B., VERBYLA, A., and THOMPSON, R. Spatial analysis of multi-environment early generation variety trials 1

DAFNI, U. G. and TSIATIS, A. A. Evaluating surrogate markers of clinical outcome when measured with error 1445
DASSIOS, A. (see CROUCHLEY, R.) 161
DAVIDIAN, M. (see HIGGINS, K. M.) 19
DAVIDIAN, M. (see HU, P.) 1407
DAWSON, J. D. Sample size calculations based on slopes and other summary statistics 323
DAY, N. E. (see McKNIGHT, B.) 426
DAYANANDA, P. W. A. (see BILLARD, L.) 877
de GUNST, M. C. M. and LUEBECK, E. G. A method for parametric estimation of the number and size distribution of cell clusters from observations in a section plane 100
DEAR, K. B. G. (see LIPSITZ, S. R.) 148
DERRYBERRY, D. R. (see MURTAUGH, P. A.) 754
DHORNE, T. J. (see CAUSEUR, D. J.) 1591
DIETZ, E. (see BÖHNING, D.) 525
DIGGLE, P. J. and VERBYLA, A. P. Nonparametric estimation of covariance structure in longitudinal data 401
DIRIENZO, A. G., ZURBENKO, I. G., and CARPENTER, D. O. Time series analysis of *Aplysia* total motion activity 493
du BERGER, R. (see BELISLE, P.) 113
DUNSON, D. B. Dose-dependent number of implants and implications in developmental toxicity 558

EFFORD, M. (see PLEDGER, S.) 888
ELMES, S. (see BILLARD, L.) 877
ELSTON, D. A. Estimation of denominator degrees of freedom of F-distributions for assessing Wald statistics for fixed-effect factors in unbalanced mixed models 1085
ENGEL, B. and BUIST, W. Bias reduction of approximate maximum likelihood estimates for heritability in threshold models 1155
ENGEN, S., BAKKE, Ø., and ISLAM, A. Demographic and environmental stochasticity—concepts and definitions 840
EVANS, T. G. and HOENIG, J. M. Testing and viewing symmetry in contingency tables, with applications to readers of fish ages 620
EWELL, M. (see LIPSITZ, S. R.) 295

FALK, R. W. and KOCH, G. G. Testing a specified difference between proportions 1602
FARAGGI, D. and SIMON, R. Bayesian variable selection method for censored survival data 1475
FAY, M. P., GRAUBARD, B. I., FREEDMAN, L. S., and MIDTHUNE, D. N. Conditional logistic regression with sandwich estimators: application to a meta-analysis 195
FEDERER, W. T. Recovery of interblock, intergradient, and intervariety information in incomplete block and lattice rectangle designed experiments 471
FEWSTER, R. M. (see BORCHERS, D. L.) 1207
FINE, J. P. (see CHENG, S. C.) 219
FINKELSTEIN, D. M. (see GOGGINS, W. B.) 1498
FISCH, R. D. (see STEPHENS, D. A.) 1334
FITZGERALD, P. E. B. and KNUIMAN, M. W. Interpretation of regressive logistic regression coefficients in analyses of familial data 909
FLYER, P. A. A comparison of conditional and unconditional randomization tests for highly stratified designs 1551
FOONG, A. P. (see HEISEY, D. M.) 712
FREEDMAN, L. (see FAY, M. P.) 195
FREEMAN, S. N. (see CATCHPOLE, E. A.) 3
FRIGGE, M. L. (see NICOLAE, D. L.) 1271

GARCÍA-DORADO, A. and MARIN, J. M. Minimum distance estimation of mutational parameters for quantitative traits 1097
GEIFAND, A. (see CARLIN, B. P.) 964
GIESBRECHT, F. G. and WHITAKER, T. B. Investigations of the problems of assessing aflatoxin in peanuts 739
GILBERT, P. B., SELF, S. G., and ASHBY, M. A. Statistical methods for assessing differential vaccine protection against human immunodeficiency virus types 799
GLASER, S. (see STEWART, S. L.) 774
GOEDHART, P. W. (see BORCHERS, D. L.) 1221
GOGEL, B. (see CULLIS, B.) 1
GOGGINS, W. B., FINKELSTEIN, D. M., SCHOENFELD, D. A., and ZASLAVSKY, A. M. A Markov chain Monte Carlo EM algorithm for analyzing interval-censored data under the Cox proportional hazards model 1498
GRAUBARD, B. I. (see FAY, M. P.) 195
GRAUBARD, B. I. (see MIDTHUNE, D. N.) 1193
GRAY, S. M. and BROOKMEYER, R. Estimating a treatment effect from multidimensional longitudinal data 976
GRIMSLEY, N. (see MANGIN, B.) 88
GRYNPAS, M. (see BRACCI, P. M.) 337
GUIARD, V. Correspondence 389

HANFELT, J. J. and LIANG, K.-Y. Inference for odds ratio regression models with sparse dependent data 136
HARRIS, M. P. (see CATCHPOLE, E. A.) 33
HASOFER, A. M. (see BECKER, N. G.) 730
HAUSER, E. R. and BOEHNKE, M. Genetic linkage analysis of complex genetic traits by using affected sibling pairs 1238
HEDLEY, S. L. (see BORCHERS, D. L.) 1221
HEIMANN, G. and NEUHAUS, G. Permutational distribution of the log-rank statistic under random censorship with applications to carcinogenicity assays 168
HEISEY, D. M. and FOONG, A. P. Modelling time-dependent interaction in a time-

varying covariate and its application to rejection episodes and kidney transplant failure 712
HIBY, L. and LOVELL, P. Using aircraft in tandem formation to estimate abundance of harbour porpoise 1280
HIGGINS, K. M., DAVIDIAN, M., CHEW, G., and BURGE, H. The effect of serial dilution error on calibration inference in immunoassay 19
HOENIG, J. (see CHEN, C.-L.) 815
HOENIG, J. M. (see EVANS, T. G.) 620
HOMMEL, G. and KRUMMENAUER, F. Improvements and modifications of Tarone's multiple test procedure for discrete data 673
HORN-ROSE, P. L. (see STEWART, S. L.) 774
HU, P., TSIATIS, A. A., and DAVIDIAN, M. Estimating the parameters in the Cox model when covariate variables are measured with error 1407
HUANG, X., CHEN, S., and SOONG, S.-j. Piecewise exponential survival trees with time-dependent covariates 1420
HUANG, Y.-C. and WONG, W.-K. Sequential construction of multiple-objective optimal designs 1388
HUFFER, F. W. and WU, H. Markov chain Monte Carlo for autologistic regression models with application to the distribution of plant species 509
HUGGINS, R. M. and LOESCH, D. Z. On the analysis of mixed longitudinal growth data 583
HUTCHINSON, T. P. and CAIRNS, D. Correspondence 788

IBRAHIM, J. G. (see KLEINMAN, K. P.) 265
IBRAHIM, J. G. (see KLEINMAN, K. P.) 921
IBRAHIM, J. G. (see LIPSITZ, S. R.) 1002
ISLAM, A. (see ENGEN, S.) 840
IVANOVA, A. (see BERGER, V. W.) 1541

JENSEN, C. S. and SHEEHAN, N. Problems with determination of noncommunicating classes for Monte Carlo Markov chain applications in pedigree analysis 416
JOLLIFFE, A. (see JOLLIFFE, I. T.) 792
JOLLIFFE, I. T. and JOLLIFFE, A. Correspondence 792
JOLY, P., COMMENGES, D., and LETENNEUR, L. A penalized likelihood approach for arbitrarily censored and truncated data: application to age-specific incidence of dementia 185
JOSEPH, L. (see BELISLE, P.) 113

KADANE, J. B. (see CARLIN, B. P.) 964
KALBFLEISCH, J. D. (see NEUHAUS, J. M.) 638
KIM, H. T., and TRUONG, Y. K. Nonparametric regression estimates with censored data: Local linear smoothers and their application 1434
KIM, M. Y. (see LEE, E. W.) 1638
KLEINMAN, K. P. and IBRAHIM, J. G. A semiparametric Bayesian approach to the random effects model 921
KLEINMAN, K. P., IBRAHIM, J. G., and LAIRD, N. M. A Bayesian framework for intent-to-treat analysis with missing data 265
KNUIMAN, M. W. (see FITZGERALD, P. E. B.) 909
KOCH, G. G. (see FALK, R. W.) 1602
KONG, A. (see NICOLAE, D. L.) 1271
KORN, E. L. (see MIDTHUNE, D. N.) 1193
KRONMAL, R. A. (see LIN, D. Y.) 948
KROONENBERG, P. M. (see van EEUWIJK, F. A.) 1315
KRUMMENAUER, F. (see HOMMEL, G.) 673
KUNSELMAN, A. R. (see TEN HAVE, T. R.) 367
KUTNER, M. H. (see TAN, M.) 682

LAIRD, N. M. (see KLEINMAN, K. P.) 265
LAIRD, N. M. (see LIPSITZ, S. R.) 148
LANDIS, J. R. (see TEN HAVE, T. R.) 367
LEE, E. W. and KIM, M. Y. The analysis of correlated panel data using a continuous-time Markov model 1638
LEE, S.-Y. and WOLFE, R. A. A simple test for independent censoring under the proportional hazards model 1176
LEISENRING, W. and PEPE, M. S. Regression modelling of diagnostic likelihood ratios for the evaluation of medical diagnostic tests 444
LÉON, L. F. and TSAI, C.-L. Assessment of model adequacy for Markov regression time series models 1165
LESAFFRE, E. and VERBEKE, G. Local influence in linear mixed models 570
LETENNEUR, L. (see JOLY, P.) 185
LEUNG, D. H.-Y. (see WANG, Y.-G.) 243
LI, H., YANG, P., and SCHWARTZ, A. G. Analysis of age of onset data from case–control family studies 1030
LIANG, K.-Y. (see HANFELT, J. J.) 136
LIN, D. Y., PSATY, B. M., and KRONMAL, R. A. Assessing the sensitivity of regression results to unmeasured confounders in observational studies 948
LIPSITZ, S. R. and IBRAHIM, J. G. Estimating equations with incomplete categorical covariates in the Cox model 1002
LIPSITZ, S. R., DEAR, K. B. G., LAIRD, N. M., and MOLENBERGHS, G. Tests for homogeneity of the risk difference when data are sparse 148
LIPSITZ, S. R., PARZEN, M., and EWELL, M. Inference using conditional logistic regression with missing covariates 295
LIU, Q. An order-directed score test for trend in ordered $2 \times K$ tables 1147
LOESCH, D. Z. (see HUGGINS, R. M.) 583
LOUGHIN, T. M. and SCHERER, P. N. Testing for association in contingency tables with multiple column responses 630
LOVELL, P. (see HIBY, L.) 1280
LUEBECK, E. G. A. (see de GUNST, M. C. M.) 100
LUI, K.-J. Interval estimation of the risk ratio between a secondary infection, given a primary infection, and the primary infection 706
LUNN, M. Applying k-sample tests to conditional probabilities for competing risks in a clinical trial 1662

MacGIBBON, B. (see BELISLE, P.) 113
MACK, Y. P. and QUANG, P. X. Kernel methods in line and point transect sampling 606
MANATUNGA, A. K. (see CHEN, M.-H.) 1348
MANGIN, B., THOQUET, P., and GRIMSLEY, N. Pleiotropic QTL analysis 88
MARIN, J. M. (see GARCÍA-DORADO, A.) 1097
MARTINUSSEN, T. and SORENSEN, T. I. A. Age-dependent U-shaped risk functions and Aalen's additive risk model 989
MATTHEWS, J. N. S. (see MEHRABI, Y.) 1398
McGORRAY, S. (see McKNIGHT, B.) 426
McKNIGHT, B., TIERNEY, C., McGORRAY, S. P., and DAY, N. E. Likelihood-based inference for the genetic relative risk based on affected-sibling-pair marker data 426
McSHANE, P. Correspondence 1673
MEHRABI, Y. and MATTHEWS, J. N. S. Implementable Bayesian designs for limiting dilution assays 1398
MEHTA, C. R., PATEL, N. R., and SENCHAUDHURI, P. Exact power and sample-size computations for the Cochran–Armitage trend test 1615
MENARD, F. (see VIENNET, G.) 304
MIDTHUNE, D. N. (see FAY, M. P.) 195
MIDTHUNE, D. N., KORN, E. L., and GRAUBARD, B. I. Correspondence 1193
MINAMI, M. and SHIMIZU, K. Estimation for a common correlation coefficient in bivariate normal distributions with missing observations 1136
MOLENBERGHS, G. (see BUYSE, M.) 1014
MOLENBERGHS, G. (see LIPSITZ, S. R.) 148
MONOD, H. (see AZAÏS, J.-M.) 1374
MORGAN, B. J. T. (see CATCHPOLE, E. A.) 33
MORRELL, C. H. Likelihood ratio testing of variance components in the linear mixed-effects model using restricted maximum likelihood 1560
MURTAUGH, P. A. and DERRYBERRY, D. R. Models of connectance in food webs 754

NAM, J. Power and sample size for stratified prospective studies using the score method for testing relative risk 331
NAVIDI, W. Bidirectional case-crossover designs for exposures with time trends 596
NETTLETON, D. and PRAESTGAARD, J. Interval mapping of quantitative trait loci through order-restricted inference 74
NEUHAUS, G. (see HEIMANN, G.) 168
NEUHAUS, J. M. and KALBFLEISCH, J. D. Between- and within-cluster covariate effects in the analysis of clustered data 638
NEWMAN, K. B. State-space modeling of animal movement and mortality with application to salmon 1290
NICOLAE, D. L., FRIGGE, M. L., COX, N. J., and KONG, A. Discussion 1271

O'HARA HINES, R. J. Comparison of two covariance structures in the analysis of clustered polytomous data using generalized estimating equations 312
OLKIN, I. and SAMPSON, A. Comparison of meta-analysis versus analysis of variance of individual patient data 317
OLSON, J. M. Discussion of Teng and Siegmund article 1266

PAN, W. and CHAPPELL, R. Estimating survival curves with left-truncated and interval-censored data under monotone hazards 1053
PARK, C. G. (see PARK, T.) 1645
PARK, T. An approach to categorical data with nonignorable nonresponse, 1579
PARK, T., SHIN, D. W., and PARK, C. G. A generalized estimating equations approach for testing ordered group effects with repeated measurements 1645
PATEL, N. R. (see MEHTA, C. R.) 1615
PARZEN, M. (see LIPSITZ, S. R.) 295
PEPE, M. S. (see LEISENRING, W.) 444
PEPE, M. S. Three approaches to regression analysis of receiver operating characteristic curves for continuous test results 124
PERMUTT, T. (see BERGER, V. W.) 1541
PETERSEN, J. H. An additive frailty model for correlated life times 646
PLANTE, N., RIVEST, L.-P., and TREMBLAY, G. Stratified capture–recapture estimation of the size of a closed population 47
PLEDGER, S. and BULLEN, L. Tests for mate and nest fidelity in birds with application to little blue penguins (*Eudyptula minor*) 61
PLEDGER, S. and EFFORD, M. Correction of bias due to heterogeneous capture probability in capture–recapture studies of open populations 888
POLLOCK, K. H. (see CHEN, C.-L.) 815
PRAESTGAARD, J. (see NETTLETON, D.) 74
PRENTICE, R. L. (see ANDERSON, A. B.) 1527
PROROK, P. C. (see XU, J.-L.) 859
PSATY, B. M. (see LIN, D. Y.) 948
PULKSTENIS, E. P. (see TEN HAVE, T. R.) 367

QUAN, H. (see SHIH, W. J.) 782
QUANG, P. X. (see MACK, Y. P.) 606

RIVEST, L.-P. (see PLANTE, N.) 47
RIVEST, L.-P., COUTURIER, S., and CRÉPEAU, H. Statistical methods for estimating caribou abundance using post-calving aggregations detected by radio telemetry 865
RUSSELL, K. E. (see THALL, P. F.) 251
RYAN, L. M. (see WELLER, E. A.)

SAMPSON, A. (see OLKIN, I.) 317
SARGENT, D. J. A general framework for random effects survival analysis in the Cox proportional hazards setting 1486
SATO, T. Correspondence 391
SCHERER, P. N. (see LOUGHIN, T. M.) 630
SCHINDLER, H. (see BAUMGARTNER, W.) 1129
SCHLATTMANN, P. (see BÖHNING, D.) 525
SCHWARTZ, A. G. (see LI, H.) 1030
SEE, K. and BAILER, A. J. Added risk and inverse estimation for count responses in reproductive aquatic toxicology studies 67
SELF, S. G. (see GILBERT, P. B.) 799

SENCHAUDHURI, P. (see MEHTA, C. R.) 1615
SHEEHAN, N. (see JENSEN, C. S.) 416
SHIH, J. H. Modeling multivariate discrete failure time data 1115
SHIH, W. J. and QUAN, H. Stratified testing for treatment effects with missing data 782
SHIMIZU, K. (see MINAMI, M.) 1136
SHIN, D. W. (see PARK, T.) 1645
SHOENFELD, D. A. (see GOGGINS, W. B.) 1498
SHULTS, J. and CHAGANTY, N. R. Analysis of serially correlated data using quasi-least squares 1622
SIEGMUND, D. (see TENG, J.) 1247
SIEGMUND, D., (see TENG, J.) 1275
SIMON, R. (see FARAGGI, D.) 1475
SINHA, D. Posterior likelihood methods for multivariate survival data 1463
SMALLWOOD, D. (see VARIYAM, J. N.) 1654
SNAPINN, S. M. Survival analysis with uncertain endpoints 209
SOONG, S.-j. (see HUANG, X.) 1420
SOORIYARACHCHI, M. R. and WHITEHEAD, J. A method for sequential analysis of survival data with nonproportional hazards 1072
SORENSEN, T. I. A. (see MARTINUSSEN, T.) 989
ST. LAURENT, R. T. Evaluating agreement with a gold standard in method comparison studies 537
STALLARD, N. Sample size determination for phase II clinical trials based on Bayesian decision theory 279
STEPHENS, D. A. and FISCH, R. D. Bayesian analysis of quantitative trait locus data using reversible jump Markov chain Monte Carlo 1334
STEWART, S. L., SWALLEN, K. C., GLASER, S. L., HORN-ROSE, P. L., and WEST, D. W. Adjustment of cancer incidence rates for ethnic misclassification 774
STIJNEN, T. (see VERWEIJ, P. J. M.) 1517
SWALLEN, K. C. (see STEWART, S. L.) 774

TAN, M., XIONG, X., and KUTNER, M. H. Clinical trial designs based on sequential conditional probability ratio tests and reverse stochastic curtailing 682
TEN HAVE, T. R., KUNSELMAN, A. R., PULKSTENIS, E. P., and LANDIS, J. R. Mixed effects logistic regression models for longitudinal binary response data with informative drop-out 367
TENG, J. and SIEGMUND, D. Multipoint linkage analysis using affected relative pairs and partially informative markers 1247
TENG, J. and SIEGMUND, D. Rejoinder 1275
THALL, P. F. and RUSSELL, K. E. A strategy for dose-finding and safety monitoring based on efficacy and adverse outcomes in phase I/II clinical trials 251
THOMAS, G. (see VIENNET, G.) 304
THOMPSON, R. (see CULLIS, B.) 1
THOQUET, P. (see MANGIN, B.) 88
TIERNEY, C. (see McKNIGHT, B.) 426
TREMBLAY, G. (see PLANTE, N.) 47
TRUONG, Y. K. (see KIM, H. T.) 1434
TSAI, C.-L. (see LÉON, L. F.) 1165
TSIATIS, A. A. (see DAFNI, U. G.) 1445
TSIATIS, A. A. (see HU, P.) 1407
TSODIKOV, A. A proportional hazards model taking account of long-term survivors 1508

van EEUWIJK, F. A. and KROONENBERG, P. M. Multiplicative models for interaction in three-way ANOVA, with applications to plant breeding 1315
van HOUWELINGEN, H. C. (see VERWEIJ, P. J. M.) 1517
VARIYAM, J. N., BLAYLOCK, J., and SMALLWOOD, D. Reduced-rank models for nutrition knowledge assessment 1654
VENKATRAMAN, E. S. (see YAO, T.-J.) 1183
VERBEKE, G. (see LESAFFRE, E.) 570
VERBYLA, A. (see CULLIS, B.) 1
VERBYLA, A. P. (see DIGGLE, P. J.) 401
VERWEIJ, P. J. M., van HOUWELINGEN, H. C., and STIJNEN, T. A goodness-of-fit test for Cox's proportional hazards odel based on martingale residuals 1517
VIENNET, G., MENARD, F., and THOMAS, G. Partial likelihood estimation in categorical time series with stochastic covariates 304

WALKER, S. A nonparametric approach to a survival study with surrogate endpoints 662
WALLER, L. A. (see YU, C.) 546
WANG, Y.-G. and LEUNG, D. H.-Y. An optimal design for screening trials 243
WASSMER, G. A comparison of two methods for adaptive interim analyses in clinical trials 696
WEI, L. J. (see CHENG, S. C.) 219
WEIß, P. (see BAUMGARTNER, W.) 1129
WELLER, E. A. and RYAN, L. M. Testing or trend with count data 762
WEST, D. W. (see STEWART, S. L.) 774
WHITAKER, T. B. (see GIESBRECHT, F. G.) 739
WHITEHEAD, J. (see SOORIYARACHCHI, M. R.) 1072
WILLIAMS, C. J. (see CHEN, M.-H.) 1348
WILLIAMSON, J. M. (see BARNHART, H. X.) 720
WITTKOWSKI, K. M. Correspondence 789
WOLFE, R. A. (see LEE, S.-Y.) 1176
WOLFSON, D. B. (see BELISLE, P.) 113
WONG, W.-K. (see HUANG, Y.-C.) 1388
WU, H. (see HUFFER, F. W.) 509

XIONG, X. (see TAN, M.) 682
XU, J.-L. and PROROK, P. C. Estimating a distribution function of the tumor size at metastasis 859
XUE, X. Multivariate survival data under bivariate frailty: an estimating equation approach 1631

YANG, P. (see LI, H.) 1030
YANG, S. Some scale estimators and lack-of-fit tests for the censored two-sample accelerated life model 1040
YAO, T.-J. and VENKATRAMAN, E. S. Optimal two-stage design for a series of

pilot trials of new agents 1183
YOUNG, D. J. and BHANDARY, M. Test for equality of intraclass correlation coefficients under unequal family sizes 1363
YU, C., WALLER, L. A., and ZELTERMAN, D. Discrete distributions for use in twin studies 546
ZASLAVSKY, A. M. (see GOGGINS, W. B.) 1498
ZELTERMAN, D. (see YU, C.) 546
ZHENG, Q. To use or not to use? Backward equations in stochastic carcinogenesis models 384
ZHOU, X.-H. Comparing correlated areas under the ROC curves of two diagnostic tests in the presence of verification bias 453
ZUCCHINI, W. (see BORCHERS, D. L.) 1207
ZURBENKO, I. G. (see DIRIENZO, A. G.) 493

SUBJECT INDEX, VOLUME 54

Aalen's additive hazard model, 989
Abundance estimation, 899
Accelerated life, 1040
Acceleration, 976
Acute rejection, 712
Adaptive interim analyses, 696
Additive odds ratio, 136
Adjusted p-values, 673
Aerial line transect survey, 1280
Affected relatives, 1247
Affected-sibling-pair methods, 426
Affected sibling pairs, 1238
Affirmative equivalence, 1602
Aflatoxin concentration, 739
Age dependence, 33
Age on onset, 1030
Aggregate data, 1527
Aggregation analysis, 1030
Agreement, 537
AIDS, 1445
Akaike's Information Criterion, 712
Alzheimer's disease, 976
Animal populations, 815
Aplysia, 493
Approximate conditional, 367
Approximate design, 1388
Areas under the ROC curve, 453
Assessment of exact methods, 168
Asymptotic distribution, 546
Asymptotic equivalence, 88
Asymptotic normality, 606
Asymptotic power, 331
Asymptotic power function, 1602
Asymptotic variance, 1136
Asymptotically efficient estimator, 939
Audiology, 444
Augmented designs, 471
Autoregressive process, 493
Autoregressive time series, 113
Average length, 706

Backward equation, 384
Backward induction, 279, 964
Bayes factor, 444
Bayesian, 265
Bayesian analysis, 1475
Bayesian design, 1398
Bayesian estimators, 1579
Bayesian inference, 113, 251, 1334
Bayesian methods, 1348
Bernoulli distribution, 662
Beta distribution, 161
Bias, 209, 638, 1155
Biased sampling model, 859
Binary data, 1155
Binary outcome, 909
Binary regression, 1221
Biplot, 1315
Birth and death processes, 840
Bivariate normal, 939
BLUP, 1, 471
Body mass index, 989
Bone marrow transplant, 350
Bone mineralization, 337
Bonferroni procedure, 673
Bootstrap, 630, 1183
Boundary crossing, 1061
Bowker's test, 620
Branching processes, 840
Breeding scheme, 1334
Brownian motion, 1061

C.A.MAN, 525
Cancer, 1498
Canonical variable, 88
Capture–recapture, 33, 888
Capture–recapture estimation, 47
Capture–recapture model, 865
Capture and recovery, 1290
Carcinogenesis model, 384
Carothers' simulation method, 888
Case–control designs, 596
Case–control family study, 1030
Case–control studies, 948
Case–control study, 136
Case–crossover design, 596
Catch-effort method, 815
Categorical time series, 304
Causal inference, 948
Cell population growth, 100
Censored data, 1040, 1475
Censoring, 1434
Change-in-ratio method, 815
Change-point, 113
Characteristic curve, 384
Cholesky decomposition, 1622
Cholesterol, 1654
Circadian rhythm, 493
Classification and regression trees, 1420
Clinical trial(s), 148, 251, 696, 1072
Clustered data, 444
Clustered populations, 828
Cohort studies, 948
Combining likelihoods, 815
Compartmental model, 1388
Competing risks, 219, 1662
Complete-case analysis, 295
Complete spatial randomness, 828
Complex diseases, 1238
Complex pedigrees, 416
Compositional data, 337
Compound gamma, 739
Conditional, 1551
Conditional likelihood, 638, 682
Conditional logistic regression, 136
Conditional power, 229
Conditional probability, 1662
Confidence intervals, 19, 1040
Confidence limit, 1602
Consistency, 1434
Constraint, 859
Continuation log ratio, 337
Copula models, 1030
Cormack–Jolly–Seber, 888
Correlated data, 720
Correlated errors, 401
Correlated frailty, 646
Correlated life times, 646
Correlation, 537
Corresponding parameterizations, 1602
Cost-benefit analysis, 279
Counting process(es), 219, 989, 1517
Counts, 1165
Covariate adjustment, 948
Covariates, 471
Coverage probability, 706
Cox model, 1176, 1517
Cox regression, 209, 948
Cramer–von Mises test, 1129
Cumulative hazards, 1407
Cumulative log ratio, 337
Cumulative logit model, 799
Curability, 350
Cure models, 1508

Data augmentation, 558
Data augmentation algorithms, 350
Data peeling, 1541
Data reconstruction, 730
Degrees of freedom, 1085
Demographic stochasticity, 840
Detection function, 828
Detection probabilities, 1207
Diagnostic test(s), 124, 453
Diagnostics, 570
Dietary fats, 1654
Difference in proportions, 1602
Differential trends, 471
Diffusion approximation, 840
Dilution assays, 482
Dirichlet process, 921
Discrete multivariate distribution, 546
Discrete sequential boundary, 1061
Discrete test statistics, 673
Disease resistance, 1315
Distribution of mutational effects, 1097

Dose-finding studies, 251
Dose–response, 337, 762
Double exponential power series, 899
Double regression, 1591
Double sampling, 774, 1591
Drosophila melanogaster, 1097
Dynamic programming, 243

Early stopping, 696
Ecological data, 509
Ecological studies, 1527
Efficiency, 762, 1374
Efficiency plots, 1388
ELISA, 19
EM, 453
EM algorithm, 74, 646, 1053, 1579
Empirical Bayes, 1183
Endpoint committee, 209
Environmental statistics, 509
Environmental stochasticity, 840
Epidemic data, 730
Ergodic Markov chain, 304
Estimation, 1040
Estimating equations, 1527
Exact conditional test, 1541
Exact permutation test, 1147
Exact power, 1615
Exact test(s), 426, 546, 1615
Exchangeable process, 662
Experimental cost, 1591
Exponential family, 865

Face validity, 1602
Familial aggregation study, 909
Familial risk, 136
Family-wise false positive rate, 1147
Fecundability, 161
Fertility studies, 525
Fidelity, 61
Fieller's theorem, 1014
Fisher information matrix, 1136
Food web, 754
Forward equation, 384
Frailty, 1463
Frailty model(s), 1486, 1517

Gamma distribution, 482
Gaussian process, 219
GEE, 1622
GEE modeling, 720
Generalized estimating equations, 195, 444, 558, 976
Generalized least squares, 19
Generalized linear model(s), 304, 482
Generalized logistic regression model, 799
Generalized multivariate hypergeometric distribution, 1147
Genetic epidemiology, 646
Genetic methods, 1238
Genetics, 426, 1238
Genome scan, 1247
Genotype-by-environment interaction, 1315
Genotype × environment interaction, 1
Gibbs sampler, 113, 921
Gibbs sampling, 416
Gold standard, 537, 1348
Goodness-of-fit test, 720, 1517
Gradient projection, 1053
Group sequential procedure, 279
Growth curves, 583

Hazard function, 185, 384
Hazards, 1053
Health effects of air pollution, 596
Hepatocarcinogenesis, 100
Heritability, 1155
Heterogeneity, 646, 1631
Heterogeneity of capture, 888
Hierarchical models, 1486
Hispanic, 774
HIV, 1498
HIV vaccine efficacy trial, 799
Horvitz–Thompson, 1221
Horvitz–Thompson estimator, 865
Human genetics, 1348
Human immunodeficiency virus, 799

Identity by descent, 1238
Ignorable missing data, 1002
Import risk assessment, 847
Independent censoring, 1176
Independent observers, 1280
Index-removal method, 815
Indifference zone, 964
Individual-based risk estimation, 67
Individual level interpretation, 161
Influential subjects, 570
Information matrix, 1388
Information time (fraction), 682
Institution effect, 148
Integer-valued autoregressive model, 113
Integer-valued time series, 113
Integrated analysis, 33
Integrated efficacy analysis, 317
Intention-to-treat, 265
Interchangeability of subscripts, 620
Interim monitoring, 964
Interregression information, 471
Interval censoring, 185
Interval estimation, 706
Intraclass correlation coefficient, 537, 1363
Inverse prediction, 888
IRREML, 1155
Islands, 416
Isotonic regression, 1147, 1645

Jonckheere–Terpstra, 762

Kalman algorithms, 1290
Kaplan–Meier estimates, 1072
Kernel estimation, 401
Kernel method, 606
Kernel weighted local regression, 401
K-function, 828
Kidney transplants, 712
k-sample test, 1662
KZ filter, 493

Lack-of-fit tests, 1040
Likelihood, 453, 1348
Likelihood ratio test, 74, 426, 939, 1363, 1560
Limiting dilution assays, 1398
Line transect, 1207, 1221
Line transect sampling, 606
Line transect survey, 828
Linear combination, 630
Linear mixed-effects model, 1560
Linear mixed model, 570
Linkage, 1247
Linkage analysis, 1238
Local linear fits, 1434
LOD score, 74
Loess, 493
Log odds, 337
Logistic regression, 720, 754, 774, 948
Logistic regression analysis, 1147
Log-linear models, 1579
Log-log link, 482
Lognormal distribution, 1527
Log-rank test, 168
Longevity, 546
Longitudinal, 265
Longitudinal data, 113, 401, 570, 921, 1622
Longitudinal data analysis, 976
Longitudinal study, 323
Loss to follow-up, 1176
Lung cancer, 1030

Mantel–Haenszel method, 136
MAPHL, 1155
Margin-based test, 1541
Marginal likelihood, 1508
Marginal models, 1115
Mark–recapture, 1207
Markov decision process, 243
Markov model, 1638
Markov regression models, 304
Markov chain Monte Carlo, 113,

1334, 1348, 1486
Martingale, 219
Martingale residuals, 1517
Matching, 61
Maximum information, 682
Maximum likelihood, 100, 1560
Maximum likelihood estimate(s), 426, 509, 1136
Maximum likelihood estimation, 1280
Maximum likelihood estimators, 1579
Maximum likelihood ratio test, 682
Maximum pest limit, 847
McNemar's test, 620
Mean and median regression functions, 1434
Mean and variance of stress, 877
Mean squared error, 209
Measurement error, 19, 1407, 1445, 1654
Meta-analysis, 525
Meta-analysis of literature, 317
Meta-analysis of patients, 317
Metastases, 859
Method comparison study, 537
Method of moments, 899
Minimum attainable p-value, 673
Minimum distance estimation, 1097
Minimum distance estimator, 1654
Missing at random, 295, 1002
Missing completely at random, 295
Missing covariate data, 295
Missing data, 265, 323, 453, 859, 909, 1475, 1498
Missing data pattern, 782
Misspecified models, 638
Mixed effects, 482
Mixed longitudinal data, 583
Mixed model, 471, 1155
Mixture distributions, 877
Mixture methods, 350
Model-based covariance estimator, 312
Model misspecification, 948
Modeling, 739
Monotone MLE, 1053
Monte Carlo, 100
Monte Carlo methods, 964, 1002
Morphological traits, 1097
Mortality, 989
Multidimensional data, 976
Multinomial data, 312
Multinomial distribution, 47
Multinomial logistic regression model, 799
Multiple imputations, 558
Multiple populations, 1527
Multiple test procedures, 673
Multiple treatment contrasts, 317
Multiplicative model, 1315
Multistage design, 279
Multivariate analysis, 88
Multivariate discrete failure times, 1115
Multivariate probit, 1654
Multivariate survival data, 1486
Mutation rate, 1097

Negative binomial, 739
Negative binomial regression, 67
Neighbour balance, 1374
Neighbour methods, 1374
Neyman–Scott Poisson process, 828
Noncompliance, 1569
Nonignorable missing data, 1579
Noninformative censoring, 1002
Nonlinear programming, 1147
Nonparametric Bayes, 921
Nonparametric estimation, 859
Nonparametric estimator, 662
Nonparametric maximum likelihood, 1407
Nonparametric maximum likelihood estimate (NPMLE), 1053
Nonparametric statistics, 1129
Nonparametric test, 426
Nonproportional hazards, 712
Nonrandomized trials, 1569
Normal random effects, 367
Nuisance parameters, 295
Null hypothesis sampling distribution, 630
Nutrition knowledge, 1654

Observational studies, 1569
Odds ratio, 909, 546, 1115
Open population models, 888
Optimal design, 1398
Optimal stopping, 279
Optimality, 243
Order restrictions, 74
Ordered categorical data, 1147, 1615
Ordered hypothesis, 1645
Ordinal data, 337
Outliers, 1165
Overdispersion, 312, 754, 865

Panel data, 1638
Partial likelihood, 304, 1508
PCBs, 493
Pearson chi-square test, 630
Pelagic behaviour, 33
Penalized likelihood, 185
Penalized partial likelihood, 712
Penalty function, 1463
Penguins, 61
Perfect surrogate, 1014
Periodic screening evaluation, 1569
Periodogram, 493
Permutational distribution, 168
Permuted block, 1551
Pest risk analysis, 847
Petersen model, 47
Phase I trial, 251
Phase II and phase III trial, 682
Phase II trial, 251
Plant breeding, 1315
Plant epidemic, 877
Point transect sampling, 606
Poisson, 762
Poisson formulation, 1631
Poisson regression, 1569
Poisson sampling, 865
Population models, 840
Positive definite matrix, 1622
Post-blocking, 471
Postrandomization stratification, 782
Power, 88, 209, 426, 1615
Power of test, 1129
PQL, 1155
Precision profile, 19
Predictive power, 229
Predictive value, 444
Pre-entry sample size, 847
Prior distribution, 1579
Prior process, 1463
Profile likelihood, 1508
Proportional hazards, 185, 229, 1072, 1445, 1508, 1517
Proportional hazards model, 1407, 1463, 1475
Pseudo-likelihood, 1115
Pseudo MLE, 939

QTL mapping, 74, 88
Quadratic function of covariates, 989
Quality of life, 976
Quantile ratio, 161
Quantitative trait locus, 1334
Quarantine, 847
Quasi-least squares, 1622
Quasi-likelihood, 136, 1165, 1631
Quasi-likelihood estimation, 1645

Random effects, 195, 265, 1527
Random effects model, 537
Random mating, 61
Random sample size, 606
Randomization, 1374, 1551
Rank-based inference, 1498
Rank test, 1129
Recapture histories, 33
Recovery data, 33
Reduced-rank models, 1654
Reducibility, 416
Regression, 1591

Regression calibration, 1407
Regressive logistic regression, 909
Reinforced random walks, 662
Rejection events, 712
Relative efficiency, 331
Relative risk, 331, 426, 1527
REML, 1, 1085
Removal method, 815
Rencontre, 61
Repeated measurements, 401
Repeated measures, 323, 482
Repeated measures analysis, 1645
Reproduction number, 730
Research synthesis, 317
Restricted maximum likelihood, 1560
Restricted maximum likelihood estimate, 1136
Reversible jump, 1334
Risk ratio, 706
Robust covariance estimator, 312
Robust variance, 195
Rotation of contrasts, 1085
Rüger test, 673

Safety monitoring, 251
Salmon smolt escapement, 47
Sample size, 331, 1615
Sample survey, 1527
Sampling distribution, 509
Sampling, 815
Satterthwaite's formula, 195
Score test, 136, 331, 720
Screening, 124
Screening clinical trials, 1183
Screening trial, 939
Self-identification, 774
Semiparametric, 989
Semiparametric method, 1407
Semiparametric models, 646
Sensitivity, 444
Sensitivity analysis, 948
Sensitivity and specificity, 124
Sequential clinical trials, 243
Sequential methods, 1072
Serial correlation, 1622
Shags, 33
Shared parameter, 367
Sieve analysis, 799
Simulation, 1348
Simulation study, 337, 1374
Simultaneous inference, 1638
Size distribution, 859
Small tumor numbers, 168
Smirnov test, 1541
Smoothed differentiation, 730
Smoothing, 401
Spatial analysis, 1
Spatial binary data, 509
Spatial modeling, 1527
Spatial statistics, 509, 1290
Specificity, 444
Spline, 185
Standardized residuals, 195
Step-down procedures, 673
Stereology, 100
Stereotype model, 799
Stochastic covariates, 304
Stochastic curtailment, 229
Stochastic integral, 877
Stochastic order, 1541
Stratification, 1551
Stratified analysis, 1602
Stratified prospective studies, 331
Stratified test, 1662
Stress assessment, 877
Subset model, 1475
Sufficient condition, 782
Surrogate endpoint, 662, 1014
Surrogate markers, 1445
Survival, 1498
Survival analysis, 229, 989, 1072, 1165, 1420, 1517
Survival distribution, 1176
Survival function, 384
Survival time, 662
Survival trees, 1420

Tarone's test, 673
Teratology, 558
Test of symmetry, 620
Test size, 782
Three-way contingency table, 620
Three-way interaction, 1315
Three-way model, 1315
Threshold, 88
Threshold model, 1155
Threshold parameter, 1165
Time dependent covariate(s), 1176, 1420
Time-dependent interaction, 712
Time-dependent nadir, 989
Time series, 1290
Time-varying covariate(s), 712, 1445
Transmission rate, 730
Treatment difference, 148
Treatment effects, 939
Treatment groups, 161
Trend analysis, 471
Trend tests, 762
True positive and false positive, 124
Truncated binomial distribution, 754
Truncation, 185
Tumor, 859
Two-sample scale problem, 1040
Two-stage design, 1183
Type I error rate, 696

Unbalanced ANOVA, 317
Unbiased variance estimation, 1602
Unconditional, 1551
Unobserved heterogeneity, 525

Validation, 1014
Validity, 1374
Variable selection, 1475
Variance component estimation, 1
Variance function estimation, 19
Variance-stabilizing transformation, 1136
Variety trial(s), 1, 1315
Variogram, 401
Verification bias, 453

Wald SPRT, 682
Wald statistic, 1085
Wald test, 136, 939
Wicksell problem, 100
Wildlife abundance estimation, 1207, 1221

z-test, 1363